

# wwPDB X-ray Structure Validation Summary Report (i)

### Oct 19, 2023 – 02:52 AM EDT

PDB ID	:	2OCU
Title	:	Structure of the complex of C-terminal lobe of bovine lactoferrin with N-(4-
		hydroxyphenyl) acetamide at 2.38 A resolution
Authors	:	Mir, R.; Singh, N.; Sinha, M.; Sharma, S.; Kaur, P.; Singh, T.P.
Deposited on	:	2006-12-21
Resolution	:	2.38  Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org A user guide is available at https://www.wwpdb.org/validation/2017/XrayValidationReportHelp with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

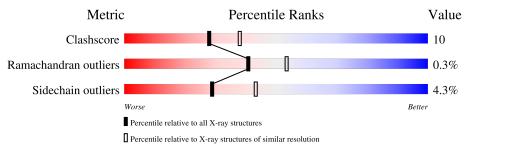
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:  $X\text{-}RAY \, DIFFRACTION$ 

The reported resolution of this entry is 2.38 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
Clashscore	141614	6082 (2.40-2.36)
Ramachandran outliers	138981	5973 (2.40-2.36)
Sidechain outliers	138945	5975 (2.40-2.36)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5%

Note EDS was not executed.

Mol	Chain	Length		Quality of chain	
1	А	345		79%	16% · ·
2	В	3	33%	67%	
3	С	4	50%	50	)%



#### 2 O C U

# 2 Entry composition (i)

There are 10 unique types of molecules in this entry. The entry contains 3000 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

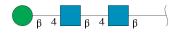
• Molecule 1 is a protein called Lactotransferrin.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
1	А	341	Total 2605	C 1622	N 454	O 508	S 21	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	565	LYS	ASN	SEE REMARK 999	UNP P24627
А	608	GLU	LYS	SEE REMARK 999	UNP P24627

• Molecule 2 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-b eta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	I	Aton	ns		ZeroOcc	AltConf	Trace
2	В	3	Total 39	C 22	N 2	0 15	0	0	0

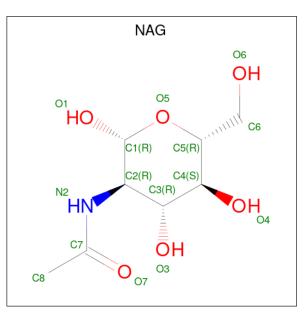
• Molecule 3 is an oligosaccharide called beta-D-mannopyranose-(1-4)-alpha-D-mannopyranos e-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-gluco pyranose.



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
3	С	4	Total         C         N         O           50         28         2         20	0	0	0



• Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{I} \\ 14 & 8 & \text{C} \end{array}$	NO 15	0	0

• Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

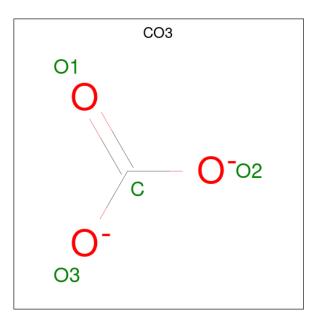
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	2	Total Zn 2 2	0	0

• Molecule 6 is FE (III) ION (three-letter code: FE) (formula: Fe).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	А	1	Total Fe 1 1	0	0

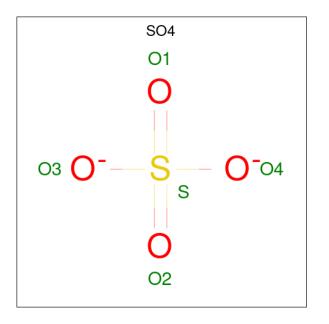
• Molecule 7 is CARBONATE ION (three-letter code: CO3) (formula: CO<sub>3</sub>).





Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	
7	А	1	Total 4	С 1	O 3	0	0

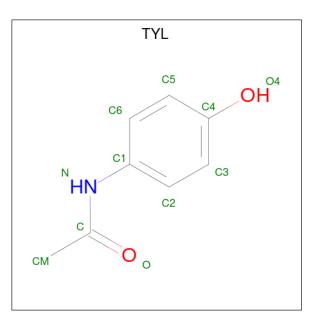
• Molecule 8 is SULFATE ION (three-letter code: SO4) (formula:  $O_4S$ ).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	
8	А	1	Total 5	0 4	S 1	0	0

• Molecule 9 is N-(4-HYDROXYPHENYL)ACETAMIDE (TYLENOL) (three-letter code: TYL) (formula:  $C_8H_9NO_2$ ).





Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	А	1	Total         C         N           11         8         1	O 2	0	0

• Molecule 10 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	А	269	Total         O           269         269	0	0

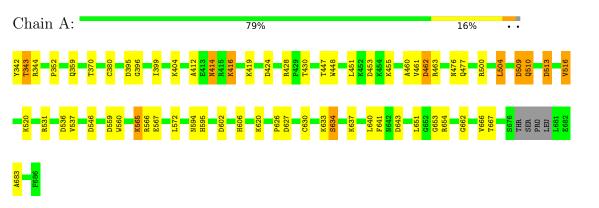


# 3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

Note EDS was not executed.

• Molecule 1: Lactotransferrin



• Molecule 2: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain B:	33%	67%	
NAG1 MAG2 BMA3			
	5		

 $\bullet \ Molecule \ 3: \ beta-D-mannopyranose-(1-4)-alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose \\ eta-D-glucopyranose \ (1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose \ (1-4)-2-acetamido-2-deoxy-beta-D-glucopyra$ 

Chain C		
Chain C:	50%	50%



## 4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	63.22Å 50.40Å 65.84Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $107.60^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	63.25 - 2.38	Depositor
% Data completeness	97.7 (63.25-2.38)	Depositor
(in resolution range)	51.1 (05.25-2.50)	Depositor
$R_{merge}$	(Not available)	Depositor
R <sub>sym</sub>	(Not available)	Depositor
Refinement program	REFMAC 5.0	Depositor
$R, R_{free}$	0.157 , $0.223$	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3000	wwPDB-VP
Average B, all atoms $(Å^2)$	36.0	wwPDB-VP



# 5 Model quality (i)

### 5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: MAN, CO3, FE, SO4, ZN, NAG, BMA, TYL

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with |Z| > 5 is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond	lengths	Bo	ond angles
	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	А	0.64	0/2653	0.88	9/3591~(0.3%)

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	А	513	ASP	CB-CG-OD2	7.51	125.06	118.30
1	А	627	ASP	CB-CG-OD2	6.73	124.36	118.30
1	А	546	ASP	CB-CG-OD2	6.57	124.21	118.30
1	А	536	ASP	CB-CG-OD2	5.96	123.67	118.30
1	А	453	ASP	CB-CG-OD2	5.47	123.22	118.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	А	2605	0	2519	49	0
2	В	39	0	34	0	0
3	С	50	0	43	2	0
4	А	14	0	13	0	0
5	А	2	0	0	0	0
6	А	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes				
7	А	4	0	0	0	0				
8	А	5	0	0	0	0				
9	А	11	0	8	4	0				
10	А	269	0	0	15	0				
All	All	3000	0	2617	53	0				

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The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

The worst 5 of 53 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:342:TYR:HD1	1:A:343:THR:H	1.00	0.97
1:A:448:TRP:HE1	1:A:477:GLN:HE22	1.11	0.93
1:A:342:TYR:HD1	1:A:343:THR:N	1.82	0.78
1:A:667:THR:HB	10:A:3248:HOH:O	1.86	0.74
1:A:653:GLY:O	1:A:654:ARG:C	2.25	0.73

There are no symmetry-related clashes.

### 5.3 Torsion angles (i)

### 5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	А	337/345~(98%)	322~(96%)	14 (4%)	1 (0%)	41 53

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type	
1	А	634	SER	



#### 5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles		
1	А	282/286~(99%)	270~(96%)	12~(4%)	29 43		

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	$\mathbf{Res}$	Type
1	А	504	LEU
1	А	509	ASP
1	А	565	LYS
1	А	510	GLN
1	А	414	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	А	477	GLN
1	А	585	GLN
1	А	594	ASN
1	А	360	GLN
1	А	359	GLN

#### 5.3.3 RNA (i)

There are no RNA molecules in this entry.

### 5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

### 5.5 Carbohydrates (i)

7 monosaccharides are modelled in this entry.



In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with |Z| > 2 is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Turne	Chain	Res	Link	Bo	ond leng	ths	В	ond ang	les
MIOI	Type	Ullaili	nes		Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z >2
2	NAG	В	1	2,1	14,14,15	0.64	0	17,19,21	1.20	2 (11%)
2	NAG	В	2	2	14,14,15	0.53	0	17,19,21	0.90	0
2	BMA	В	3	2	11,11,12	0.67	0	$15,\!15,\!17$	1.02	1 (6%)
3	NAG	С	1	3,1	14,14,15	0.78	1 (7%)	17,19,21	1.33	1 (5%)
3	NAG	С	2	3	14,14,15	0.70	1 (7%)	17,19,21	0.96	0
3	MAN	С	3	3	11,11,12	0.66	0	$15,\!15,\!17$	1.56	2 (13%)
3	BMA	С	4	3	11,11,12	0.66	0	$15,\!15,\!17$	1.33	2 (13%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	В	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	В	2	2	-	4/6/23/26	0/1/1/1
2	BMA	В	3	2	-	2/2/19/22	0/1/1/1
3	NAG	С	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	С	2	3	-	0/6/23/26	0/1/1/1
3	MAN	С	3	3	-	1/2/19/22	0/1/1/1
3	BMA	С	4	3	-	2/2/19/22	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	С	1	NAG	C1-C2	2.38	1.55	1.52
3	С	2	NAG	O5-C1	-2.09	1.40	1.43

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^{o})$	$Ideal(^{o})$
3	С	1	NAG	C1-O5-C5	3.90	117.48	112.19

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Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
3	С	3	MAN	O5-C5-C6	3.61	112.86	107.20
3	С	3	MAN	C1-O5-C5	3.60	117.06	112.19
3	С	4	BMA	C3-C4-C5	3.39	116.28	110.24
2	В	1	NAG	O5-C1-C2	-3.13	106.35	111.29

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There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	В	2	NAG	C8-C7-N2-C2
2	В	2	NAG	O7-C7-N2-C2
3	С	4	BMA	O5-C5-C6-O6
2	В	3	BMA	C4-C5-C6-O6
3	С	4	BMA	C4-C5-C6-O6

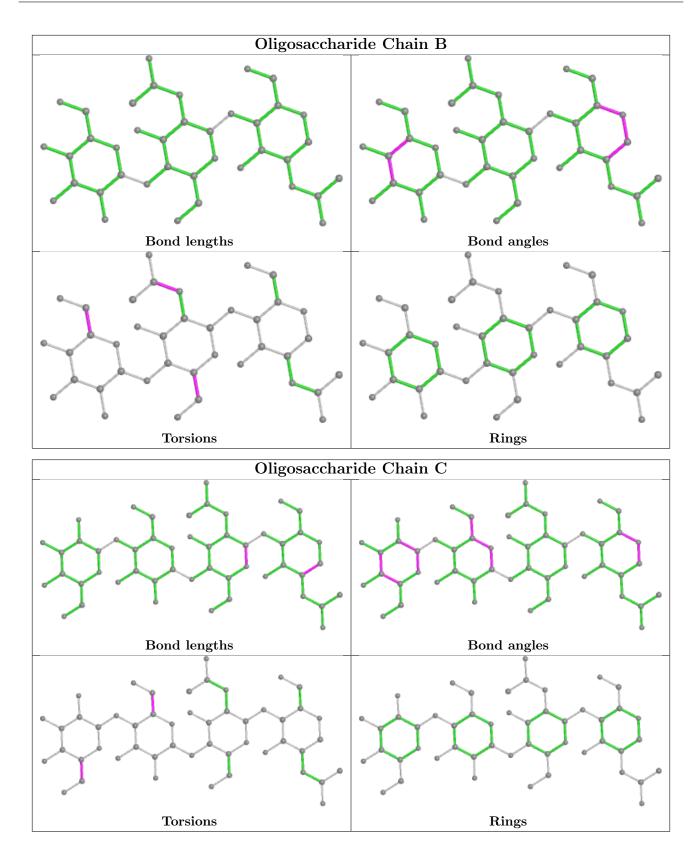
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	С	2	NAG	1	0
3	С	4	BMA	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.





### 5.6 Ligand geometry (i)

Of 7 ligands modelled in this entry, 3 are monoatomic - leaving 4 for Mogul analysis.



In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with |Z| > 2 is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mal	Mol Type Cl	Chain	Dec	s Link	Bo	Bond lengths			Bond angles		
IVIOI	туре	Chain	$\operatorname{Res}$	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z  > 2	
4	NAG	А	1001	1	14,14,15	0.47	0	$17,\!19,\!21$	1.69	2 (11%)	
8	SO4	А	2001	-	4,4,4	0.15	0	$6,\!6,\!6$	0.38	0	
9	TYL	А	3001	-	11,11,11	0.88	1 (9%)	$14,\!14,\!14$	0.52	0	
7	CO3	А	1999	6	2,3,3	0.54	0	2,3,3	1.96	1 (50%)	

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	А	1001	1	-	2/6/23/26	0/1/1/1
9	TYL	А	3001	-	-	0/4/4/4	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	А	3001	TYL	C1-N	-2.44	1.36	1.41

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
4	А	1001	NAG	C1-O5-C5	5.24	119.29	112.19
4	А	1001	NAG	O5-C5-C6	3.59	112.83	107.20
7	А	1999	CO3	O3-C-O1	2.65	126.42	119.55

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	А	1001	NAG	C4-C5-C6-O6
4	А	1001	NAG	O5-C5-C6-O6



There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	A	3001	TYL	4	0

### 5.7 Other polymers (i)

There are no such residues in this entry.

### 5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



## 6 Fit of model and data (i)

## 6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section is therefore empty.

## 6.2 Non-standard residues in protein, DNA, RNA chains (i)

EDS was not executed - this section is therefore empty.

## 6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

## 6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.

